Figure 1

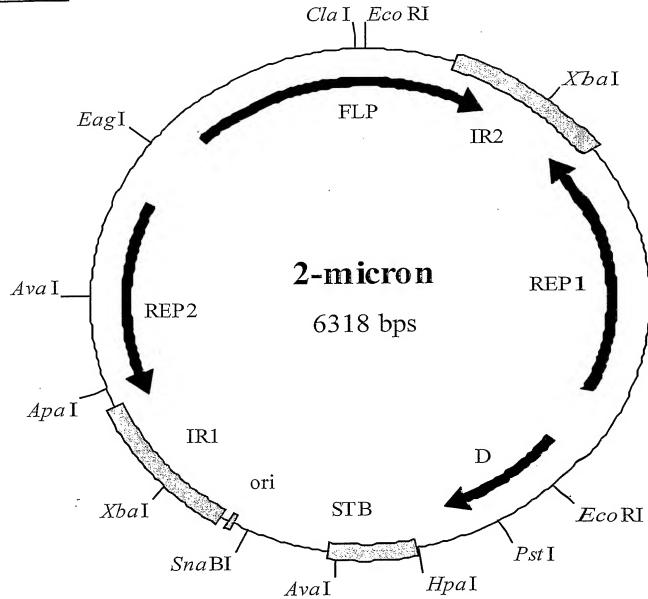
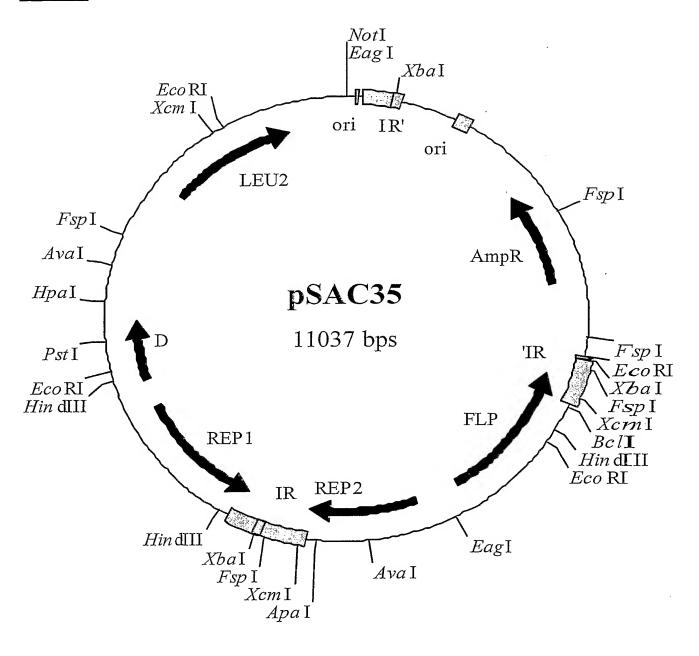


Figure 2



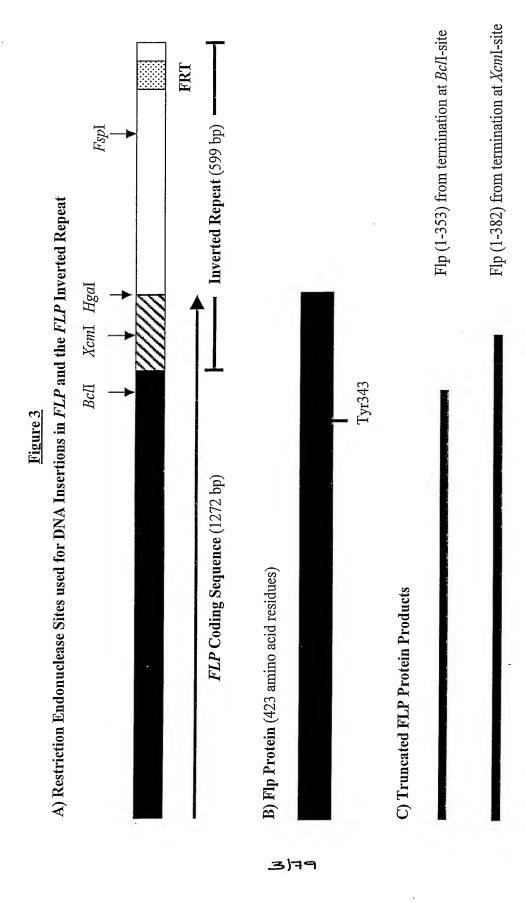


Figure 4

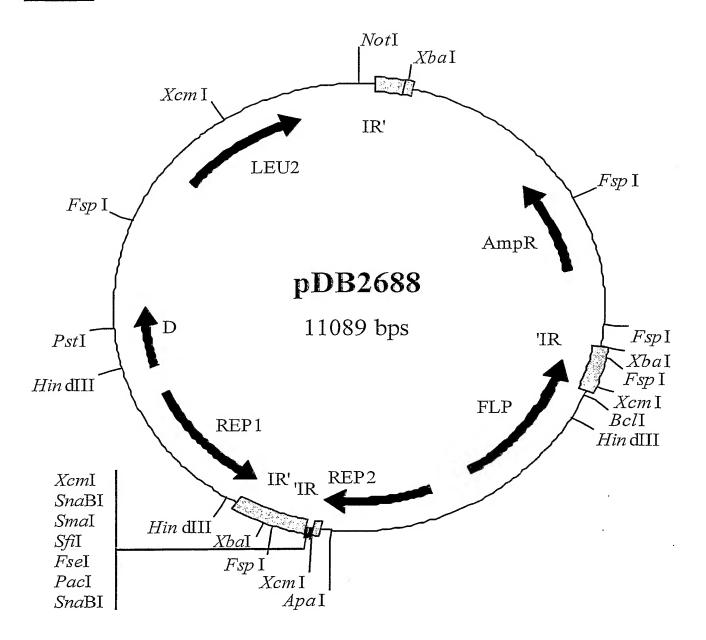


Figure 5

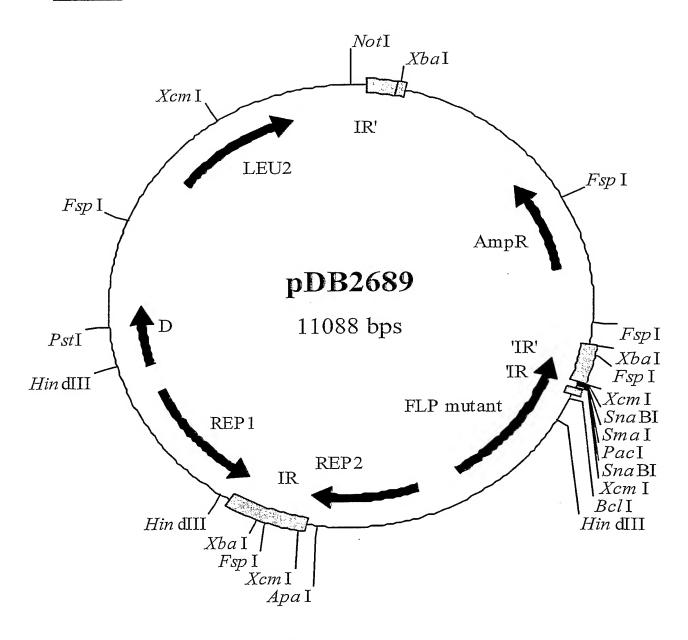


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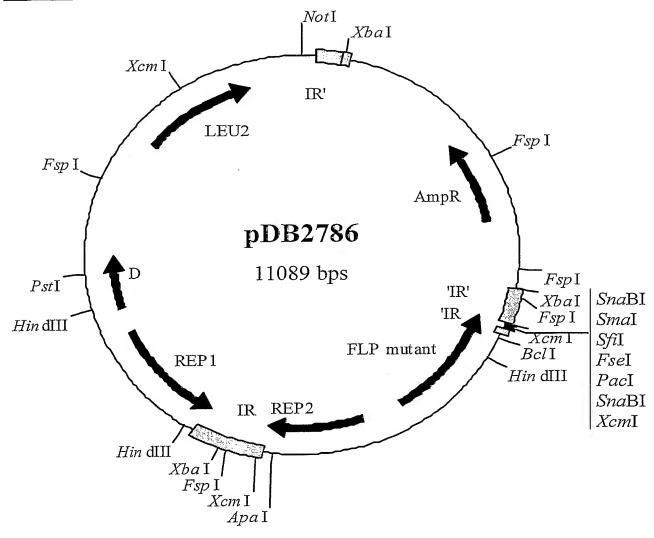


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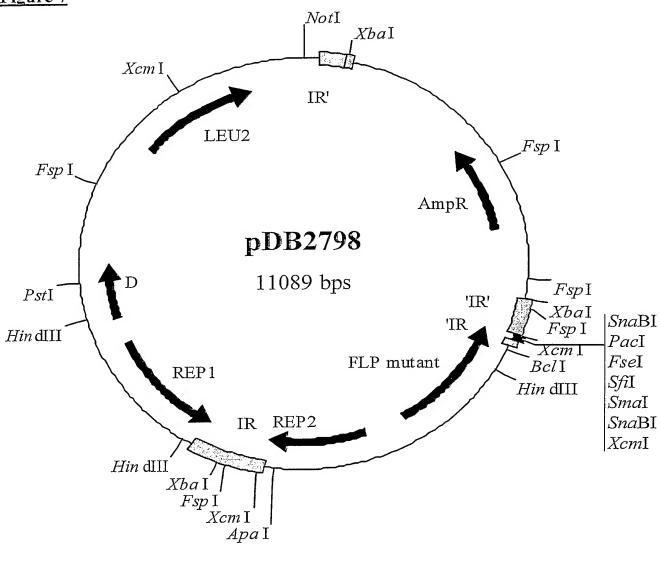


Figure 8

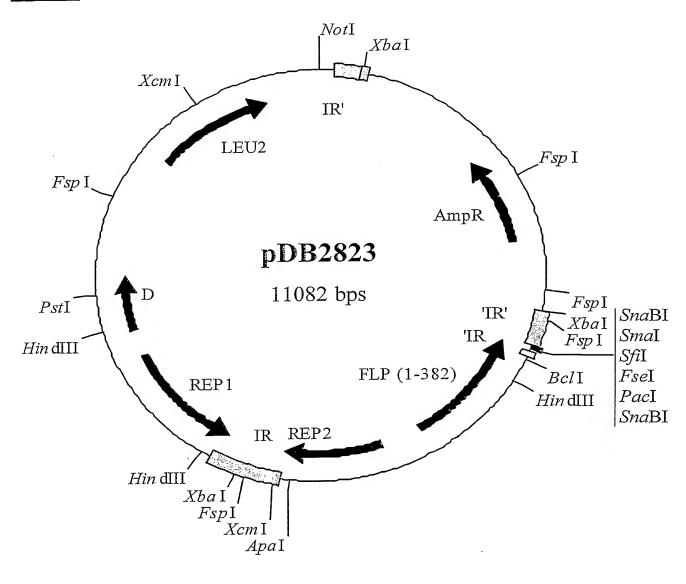


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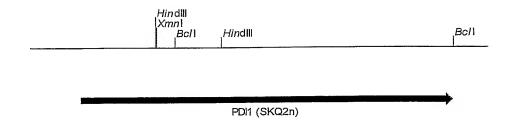


Figure 10

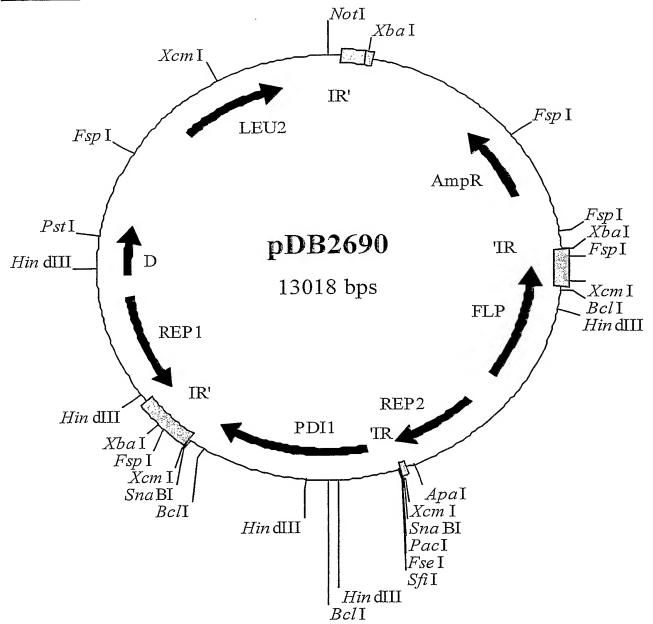
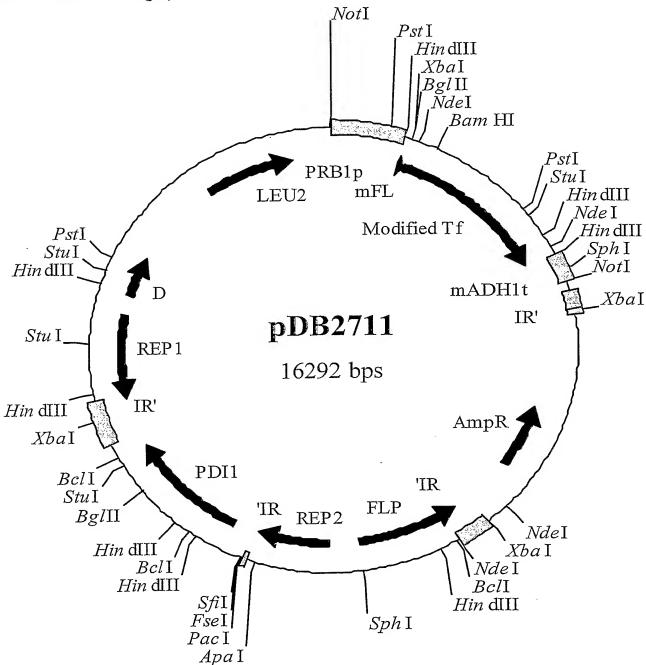


Figure 11

 $mFL = modified HSA(pre)/MF\alpha1(pro)$ fusion leader sequence



5

Figure 12

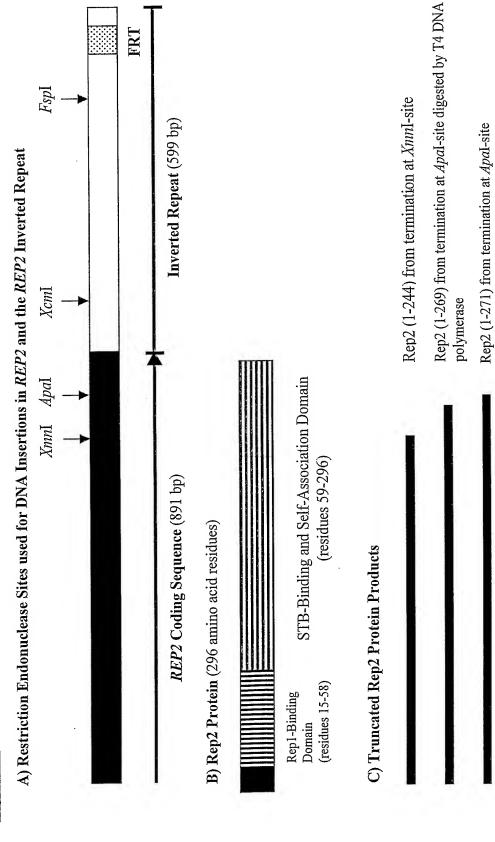


Figure 13

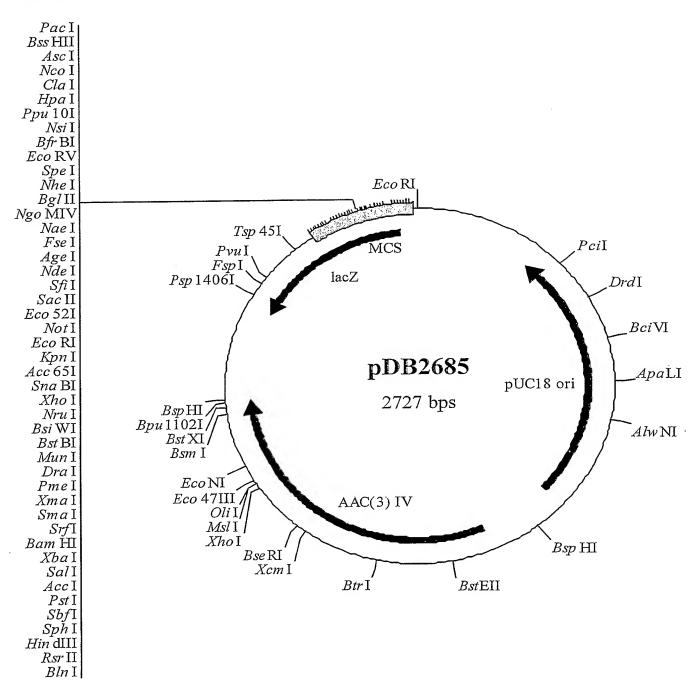


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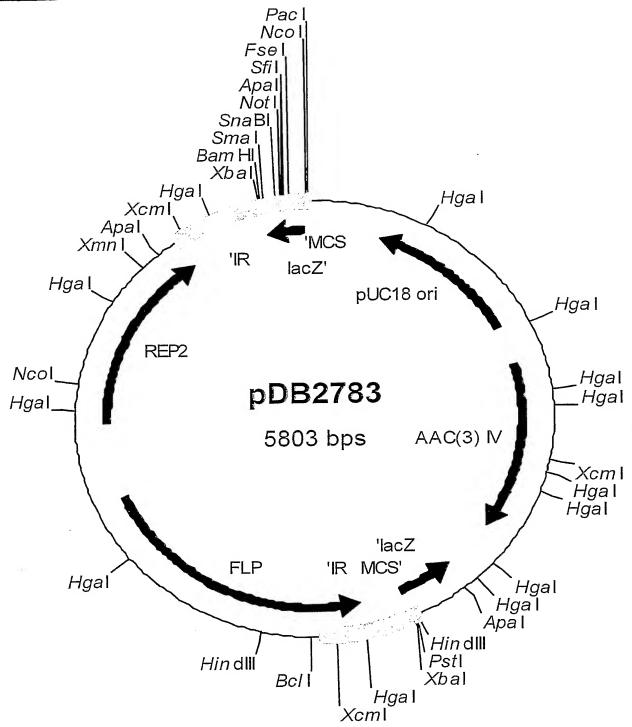


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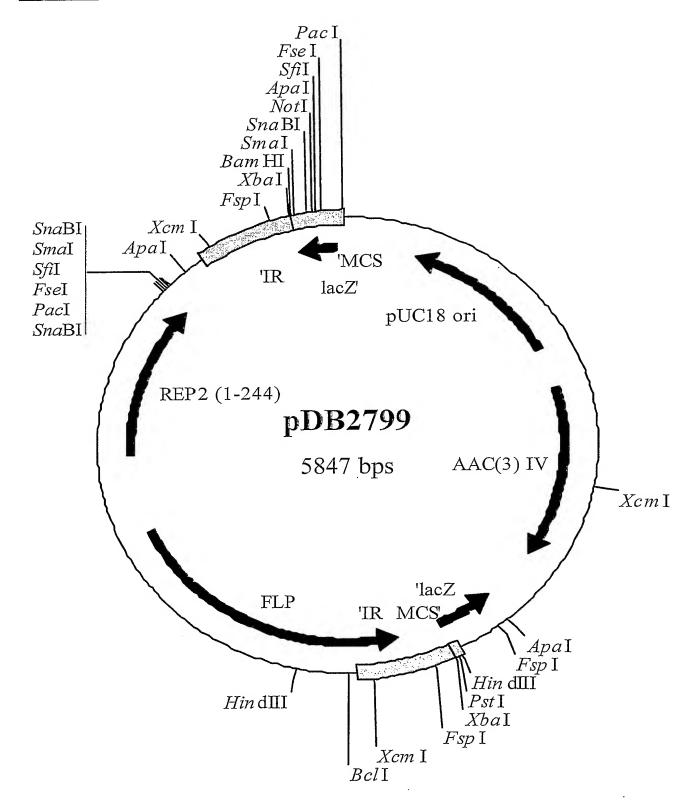


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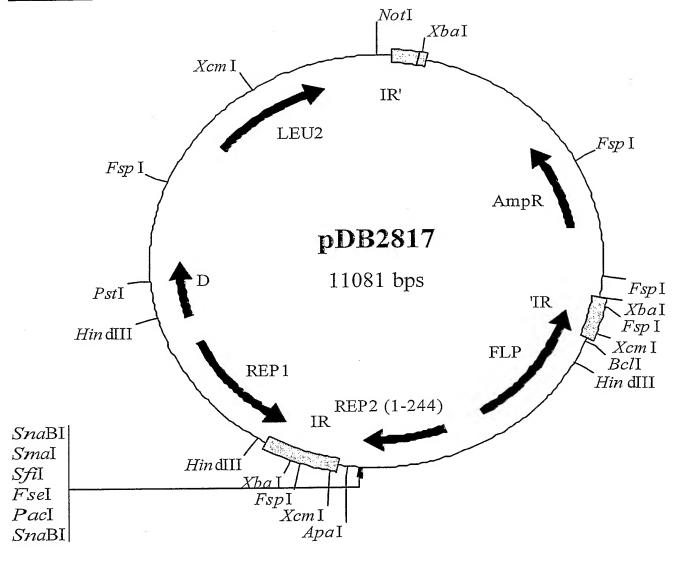


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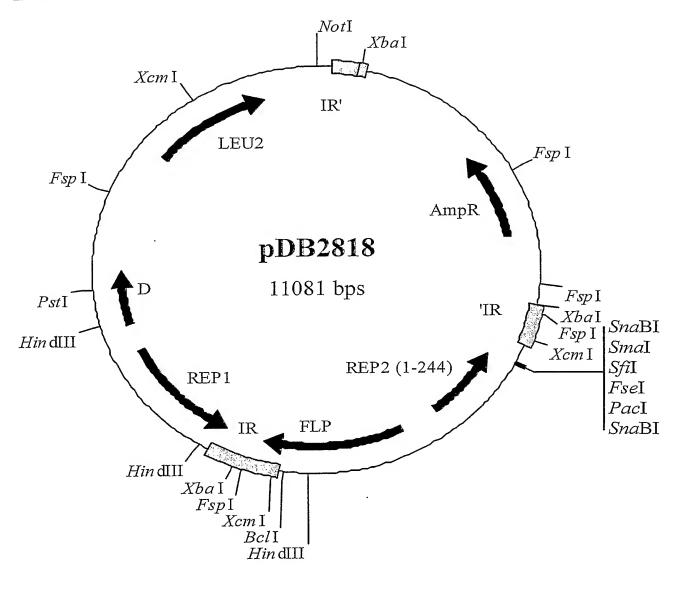


Figure 18

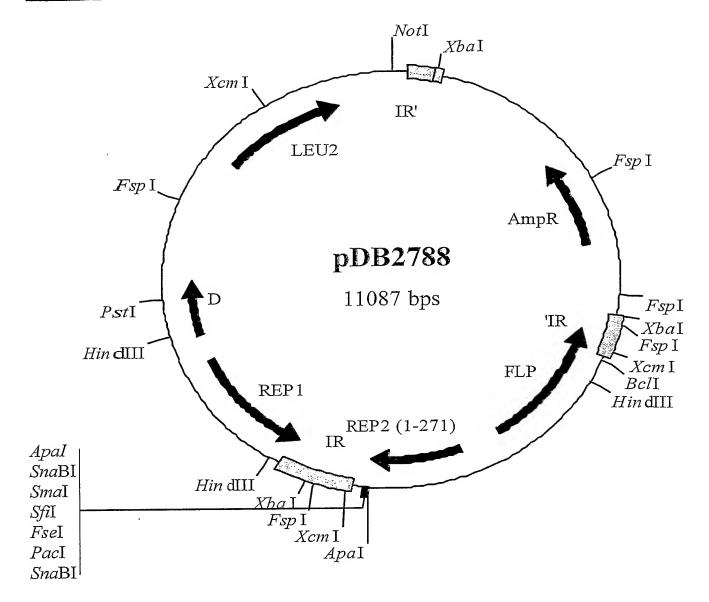


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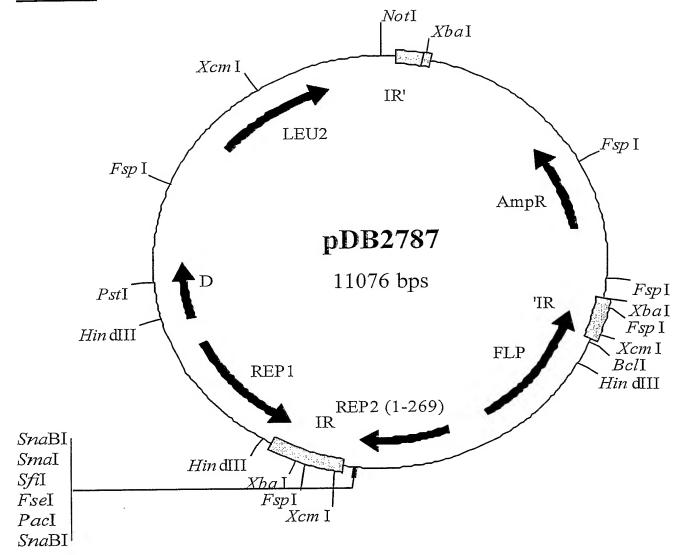


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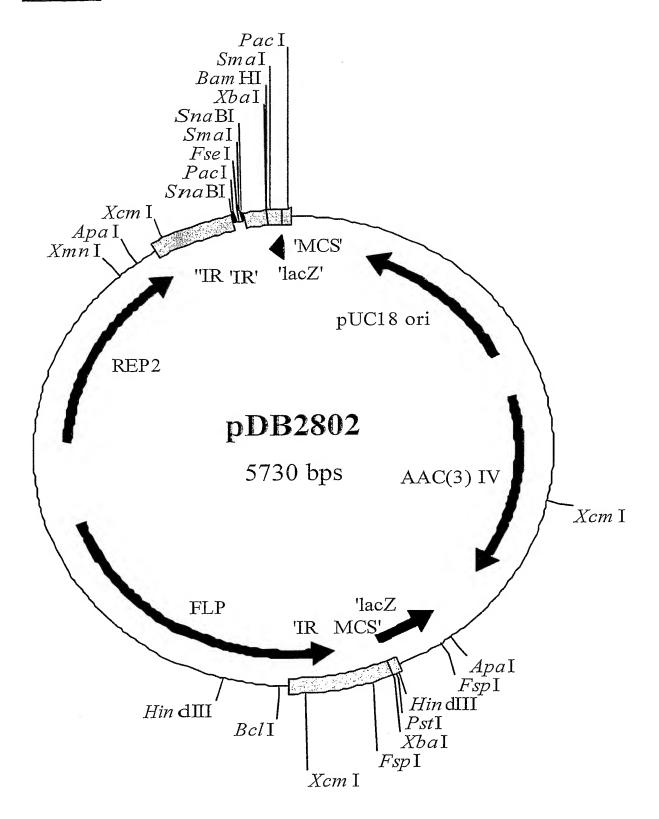


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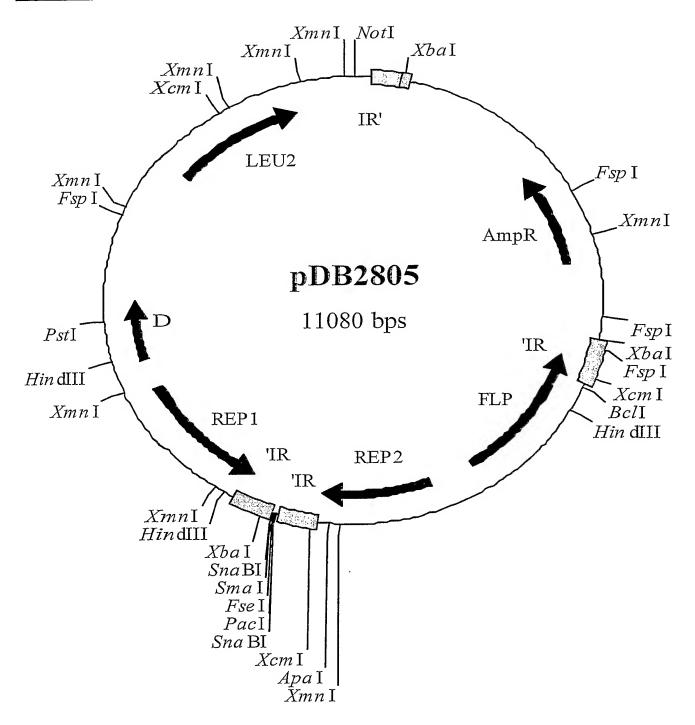


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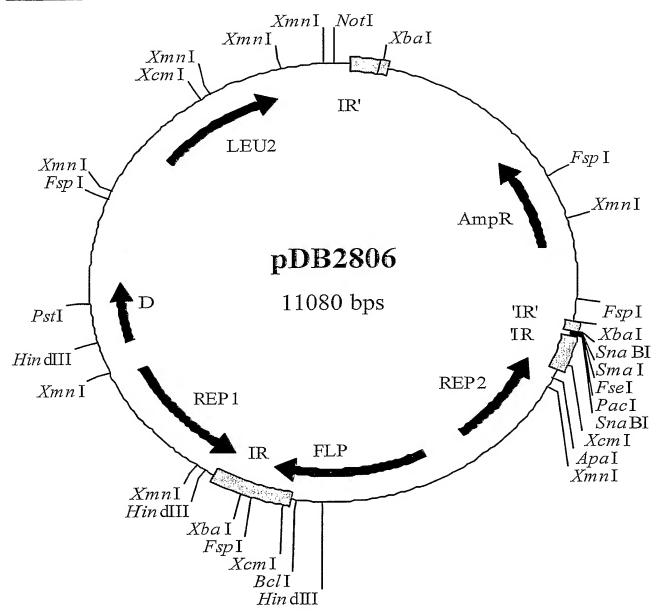


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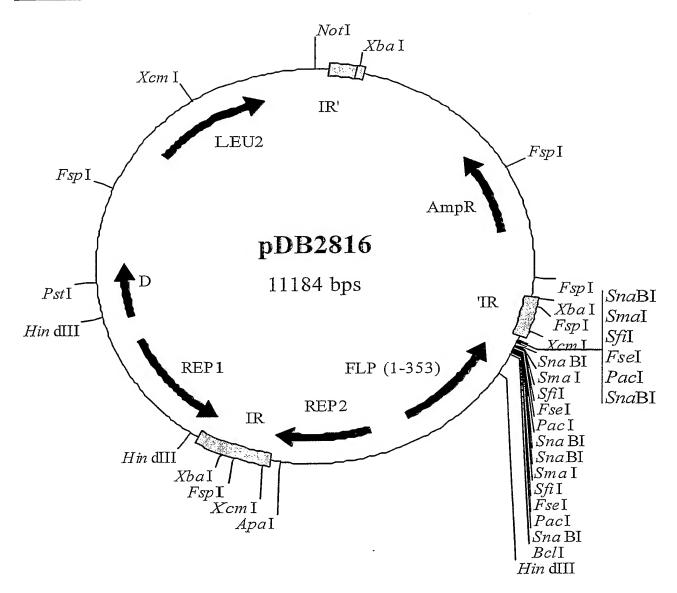


Figure 24

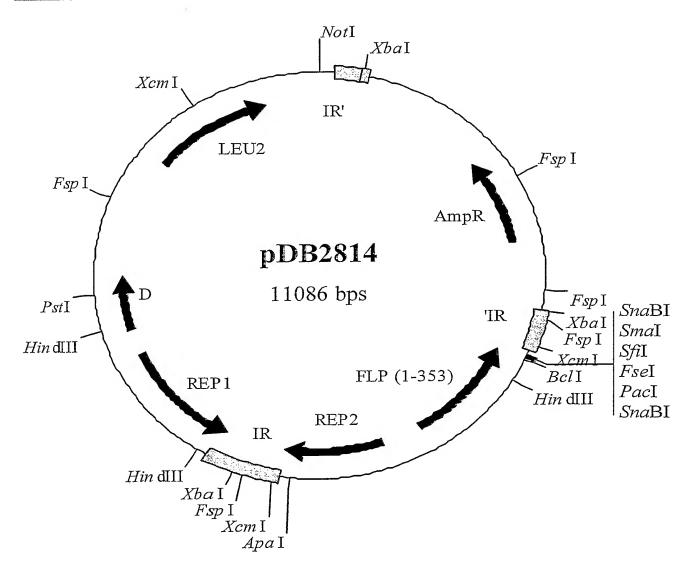


Figure 25

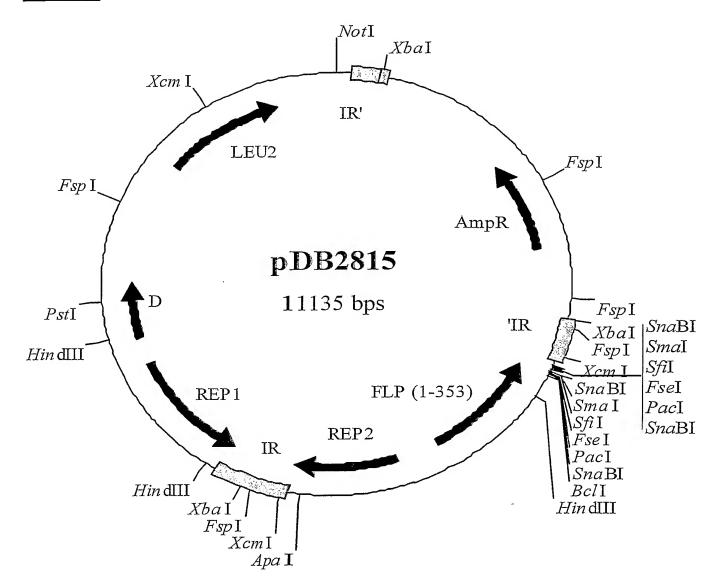


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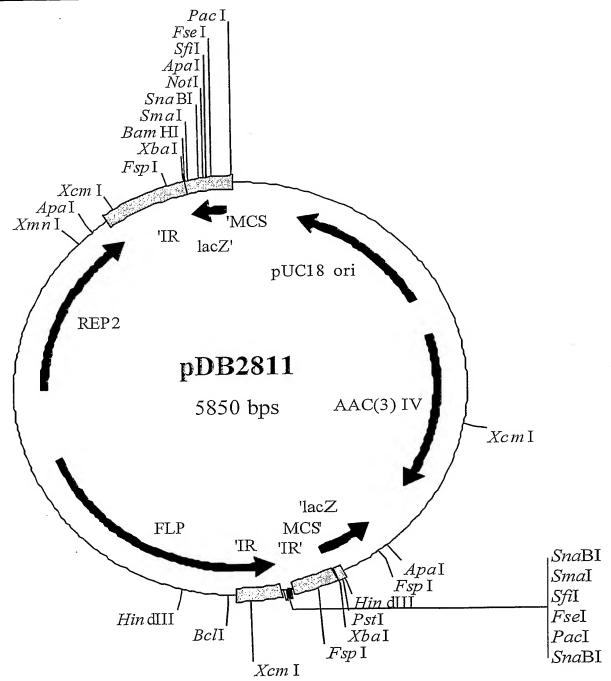


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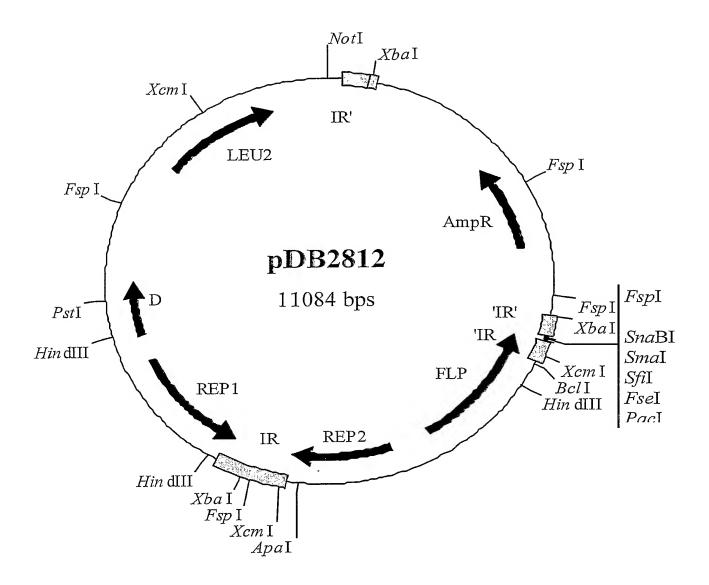


Figure 28

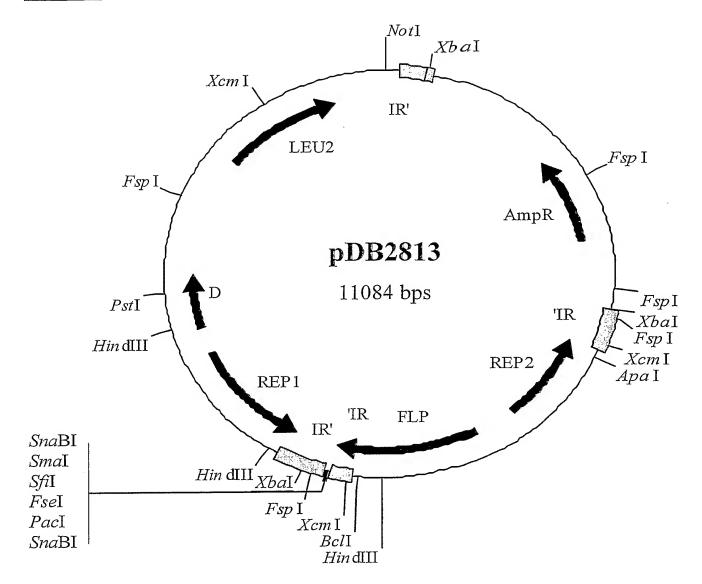


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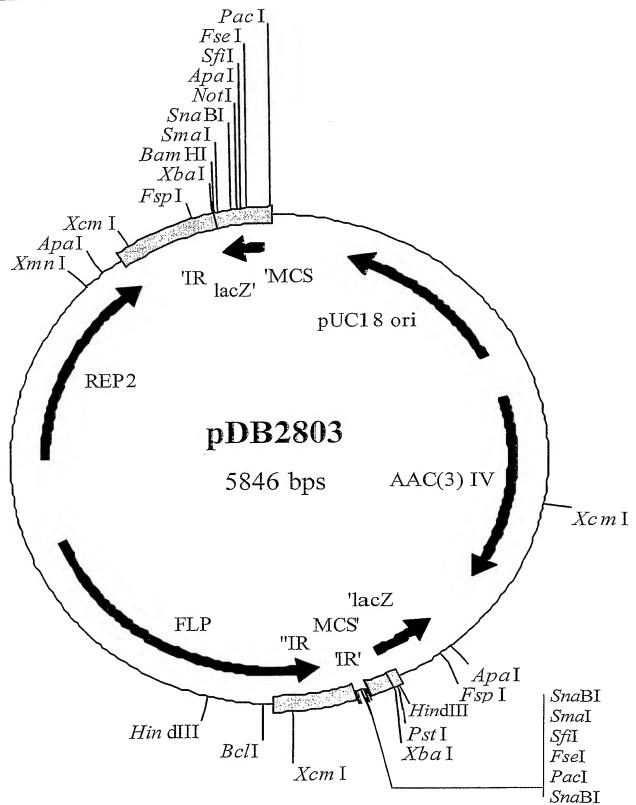


Figure 30

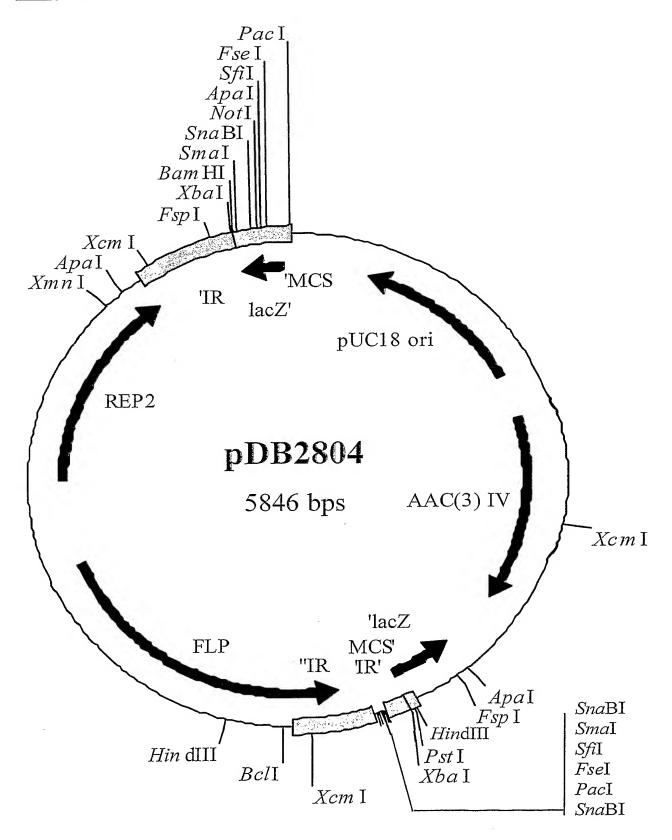


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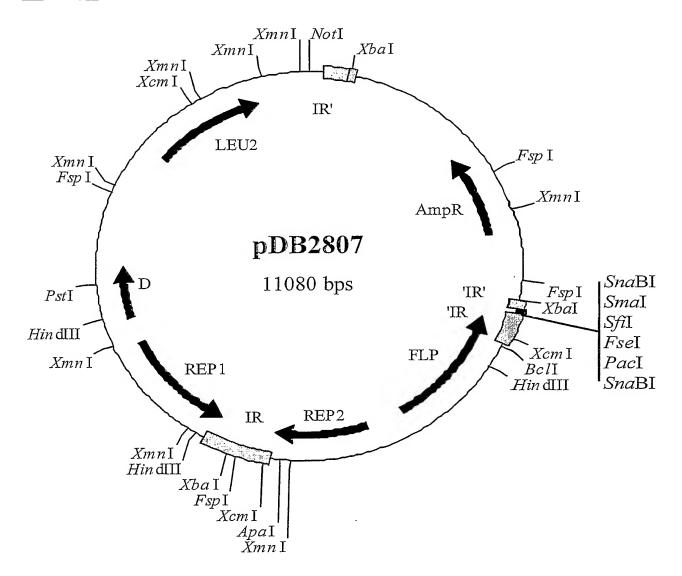
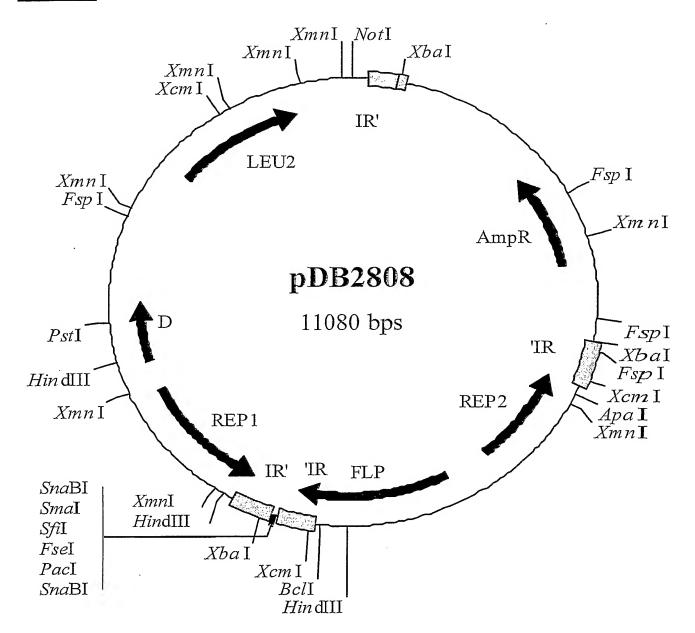


Figure 32



igure 33A

Table 3 (part 1)

Plasmid	Insertion Site	Insertion Site Details	2µm	Initial	Leu	Leucine Prototrophs	sqdo.
	one		Form	00900	Number	%	Average
pSAC35	1	1	В	0.074	100/100	100%	
pSAC35		1	В	0.068	86/56	%16	%66
pDB2818	XmnI	REP2 (1-244)	A	0.062	32/100	32%	
pDB2818	XmmI	REP2 (1-244)	A	0.059	52/100	52%	42%
pDB2787	Apal/T4 pol.	REP2 (1-269)	В	0.054	34/100	34%	
pDB2787	Apal/T4 pol.	REP2 (1-269)	В	0.084	45/100	45%	45%
pDB2788	Apal	REP2 (1-271)	В	990.0	23/100	23%	
pDB2788	Apal	REP2 (1-271)	В	0.051	43/100	43%	33%

Figure 33B

Table 3 (part 2)

Plasmid	Insertion Site	Insertion Site Details	2µm Form	Initial OD ₆₀₀	Leu	Leucine Prototrophs	sydo
					Number	%	Average
pDB2688	Xcml	Inverted Repeat	В	0.055	100/100	100%	
PDB2688	Xcml	Inverted Repeat	В	990.0	100/100	100%	100%
pDB2806	Fspl	Inverted Repeat	А	0.073	100/100	100%	
pDB2806	FspI	Inverted Repeat	A	0.070	100/100	100%	100%
pDB2817	Xmnl	REP2 (1-244)	В	0.063	36/100	36%	
pDB2817	Xmml	REP2 (1-244)	В	0.082	34/100	34%	35%
pDB2805	Fspl	Inverted Repeat	В	0.069	100/100	100%	
pDB2805	FspI	Inverted Repeat	В	0.078	100/100	100%	100%
pDB2814	BcII	FLP (1-353), 1× Insert	В	0.080	69/100	%69	
pDB2814	BcII	FLP (1-353), 1× Insert	В	0.057	64/100	64%	67%
pDB2815	BcII	FLP (1-353), 2× Insert	В	0.067	70/100	%0 <i>L</i>	
pDB2815	BcII	FLP (1-353), 2× Insert	В	0.068	64/100	64%	67%

igure 33C

Table 3 (part 3)

Plasmid	Insertion Site	Insertion Site Details	2µm Form	Initial OD ₆₀₀	nen	Leucine Prototrophs	ophs
					Number	%	Average
pDB2816	BcII	FLP (1-353), 3× Insert	В	0.069	67/100	67%	ì
pDB2816	BcII	FLP (1-353), 3× Insert	В	0.056	81/100	81%	/4%
pDB2689	XcmI	C-terminal FLP Mutant (FLP 1-384, plus 56 other residues)	В	0.054	73/100	73%	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \
pDB2689	XcmI	C-terminal FLP Mutant (FLP 1-384, plus 56 other residues)	В	0.056	77/100	77%	/3%
pDB2786	XcmI	C-terminal FLP Mutant (FLP 1-384, plus 14 other residues)	В	0.079	73/100	73%	70127
pDB2786	XcmI	C-terminal FLP Mutant (FLP 1-384, plus 14 other residues)	В	0.052	61/100	61%	%/0
pDB2823	XcmI	FLP (1-382)	В	0.071	70/100	70%	
pDB2823	Xcml	FLP (1-382)	В	0.055	57/100	57%	64%

igure 33D

Table 3 (part 4)

Plasmid	Insertion	Insertion Site Details	711m	Initial	neT	Leucine Prototrophs	sydo.
	Site		Form		Number	%	Average
pDB2813	Hgal	Inverted Repeat	A	0.057	100/100	100%	0
pDB2813	Hgal	Inverted Repeat	А	0.076	100/100	100%	100%
pDB2808	FspI	Inverted Repeat	A	0.058	100/100	100%	
pDB2808	FspI	Inverted Repeat	A	090.0	100/100	100%	100%
pDB2812	Hgal	Inverted Repeat	В	0.062	100/100	100%	
pDB2812	Hgal	Inverted Repeat	В	0.071	100/100	100%	100%

Figure 34

SEQ ID NO:1

AGCGCTCTGA AGACGCACTT TCAAAAAACC AAAAACGCAC CGGACTGTAA CGAGCTACTA AAATATTGCG AATACCGCTT CCACAAACAT TGCTCAAAAG TATCTCTTTG GIGCGCAGCI CGCGIIGCAI ITICGGAAAC GAAGGAAGGA CTGAAGTGAA CCATGCTAAT ACAAATGAAG AAGTTCCCTC CAGGCGAACA AGAAGTAGAG ACACAAATGC AAGAGGAGCA TATAAATTAC AAAACACCAT CACTGAGGGC CCIAAAGCGG ITCCCACGAA AAAAGGAGA GIAGCAACGA GGGIAAGGGG CAGAAAAICA CGIAAIACTI CIAGGGIAIG AICCAAIAIC ITTCATCCTA CATAAATAGA CGCATATAAG TACGCATTTA AGCATAAACA CGCACTATGC ATGGACGACA TTGAAACAGC CAAGAATCTG ACGGTAAAAG CACGTACAGC TTATAGCGTC TGGGATGTAT GTCGGCTGTT TATTGAAATG ATTGCTCCTG TTAAGGAAAG GTTTGATTCG CAATAGAAAG CAACTATACA TATTAGTCCC AATAGGTGAT AAAGGAAATG ATAGCATTGA AGGATGAGAC TAATCCAATT GAGGAGTGGC AGCATATAGA ACAGCTAAAG GGTAGTGCTG AAGGAAGCAT ACGATACCCC CICACAACCG GIAGGCCGIA GAAAACCAAA TGTACACAGT GAGIGAGIIG AAGCTGCTTT CIGIGCIAIA ICCCIAIAIA ACCIACCCAI CCACCITICG CICCITGAAC IIGCAICIAA ACICGACCIC IACAI SCICGIIIIIC GGAAACGCII IGAAGIICCI AIICCGAAGI ICCIAIICIC IAGAAAGIAI AGGAACIICA GAGCGCIIII TITGATGCTA CAGAATAACA AGCTGTTAGA TGCTCATGAG AAAAATGGAT CCAGATCGTC TTATTCATCC CGGAATCTCT AAAGGATATA TTCAATAGTT TCAATGAACT GGCGGCAGAG AATCGTTTAC AGCAAAAAA CCAGGATATG TCATAAGGCC CATGGAATCT GCGAAGATGG CGTICTICIC ATGIATAIAT ATATACAGGC AACACGCAGA TATAGGTGCG ACGTGAACAG IGAGCTGTAT TTTAGTTCCA TTTGCCTGCT GCTACCGAAA AATTGCTTAC CTGAGGTAAT CTGCCATAGA GTCGTTACCC GCTACTCTTT GACTCCAGTG CAAGAAGAGA GGATAATATC ACAGGAGGTA CTAGACTACC AGTAAACGTA AGTCTGATGA CGTATCTTCT GCAAGTCAGG CCGAGAAAGA GCTCGTAAGC ACGGAAGAAG ATGTTATGAA GGAAGATTGC TTCACAAGAA AAGATTCCAG TGATATAGAG TATAATAATA TCTAGCGCAG GTATGCTCTC ACCAGCTCCA GCATGGAATG CTATATATCT ATGTAGATAT TGGTCTTGAT ATTGGAAATG AATCTATIGC 501 601 701 801 1001 1101 1201 1301 1401 201 301 901 401

ligure 3.

SEQ ID NO:2

FGAAGACGCA CITICAAAAA ACCAAAAACG CACCGGACTG TAACGAGCTA CTAAAATAIT GCGAATACCG CTTCCACAAA CATTGCTCAA AAGTAICTCT CATACGATAC TTAAGCATAA ACACGCACTA TCAGAGGGCT TTTGAAAACC AAAAGCGCTC CGTTTGAGTA CGTTGATCCG CCACTIGIAT ATTIGGAIGA ATTITIGAGG AATTCTGAAC CAGICCIAAA ACGAGIAAAT AGGACCGGCA ATTCTTCAAG GAATACCAAT TATTAAAAGA TAACTTAGTC AGATCGTACA ATAAAGCTTT GAAGAAAAT GCGCCTTATT CAATCTTTGC TATAAAAAT GGGAAATIGG AGCGATAAGC STGCTICTGC CGTGGCCAGG ACAACGTATA CTCATCAGAT AACAGCAATA CCTGATCACT ACTTCGCACT AGTTTCTCGG TACTATGCAT ATGATCCAAT CTCATGTATA TATATATACA GGCAACACGC AGATATAGGT GCGACGTGAA CAGTGAGCTG TATGTGCGCA GCTCGCGTTG CATTTTCGGA GAAGAAGCAG TCAGTITGIG GAAAGGITIG AAAGACCITC AGGIGAGAAA AIAGCAITAI GCAATCAAGA GAGCCACATI CATGAGCTAT AATACTATCA TAAGCAATTC TCCTGCTTGG CTGAAGGAAG AAAAAGCAAC AATTCTGGAA GCCTCATTAA AGAAATTGAT TGATATIGIA AGTAGITIGC AATTACAGIT CGAATCAICG ATACTAAATT TAGGCACATA ATATTAAGAA CTCTACAT ITGCTATATA TCTCTGTGCT ATATCCCTAT ATAACCTACC CATCCACCTT TCGCTCCTTG AACTTGCATC TAAACTCGAC GGTGAAAGCA TCTGGGAGAT CACTGAGAAA AGATTCAGCG CAAGCGTTAG GGCCCAAAAT CTCACATTGG AAGACATTTG ATGACCTCAT TTCTTTCAAT GAAGGGCCTA ACGGAGTTGA CTAATGTTGT GGCAGCATAT AGAACAGCTA AAGGGTAGTG ACCTITCAIC CIACAIAAAI AGACGCAIAI AAGIACGCAI TICGGAAACG CTITGAAGII CCTATICCGA AGTICCIAIT CTCIAGAAAG IAIAGGAACI CAATTGTGGA GAGACAAAGA CTACTTTCAT TTTAGTGACA ATGCCACAAT ITGGTATAIT ATGTAAACA CCACCTAAGG TGCTTGTTCG TACAAGACGC TCTAAGTGAG CTCTTCCTAG TAATCCAGTG GACTAATCCA ATTGAGGAGT TAACGGAACA CTGATATCAC ATCACAGGAG GTACTAGACT ACTAACCTAT TTATGTTGGA TGATTACACA CCAGTTTAAA TTATTCCTTA CTATGGACAA AAACATCAAT TTAAAGCACT ATACCAATTC CTGGGAGTAA ATCAAAGGAA ATGATAGCAT TGAAGGATGA AAATAAGTAT CAAAAACTTT GATATIGICA ATAAAICACI AAAAAAATGC TAGCCACAGT TAGGATCGAT ATGGGATAAT TTTACAAAAA AATTAGTCCA CAATAAACAG AGCGCTCGTT GCGCAAGGGG CCCCCATGGA TGCCGTTCTT GTGCTGCTGA GCTGAGTTTC SAATTTACAA ATAAGGGAAA TACTTCGAGA AAATCATTTA 901 1201 1301 1401 701 801 1001 1101 601 401

Figure 36

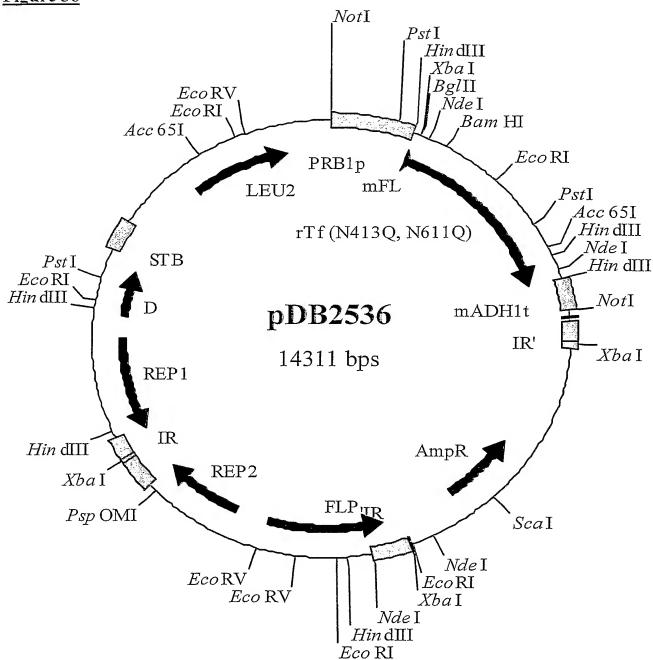


Figure 37

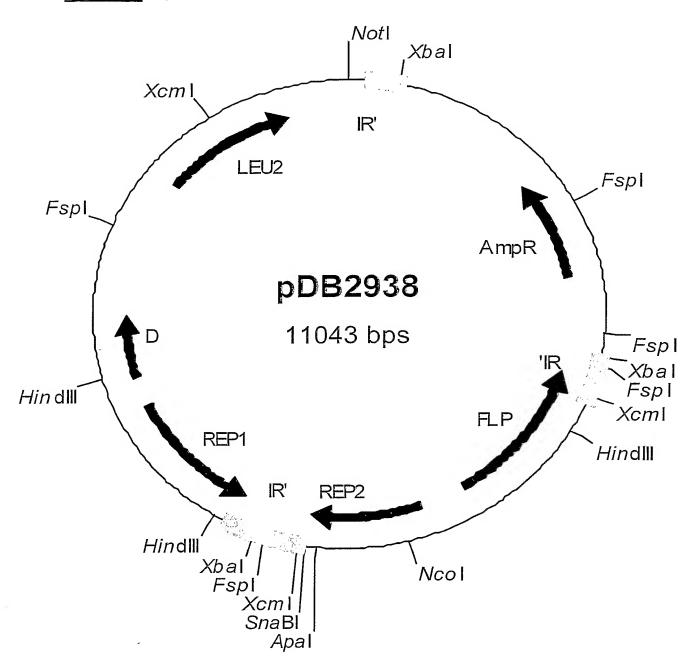


Figure 38

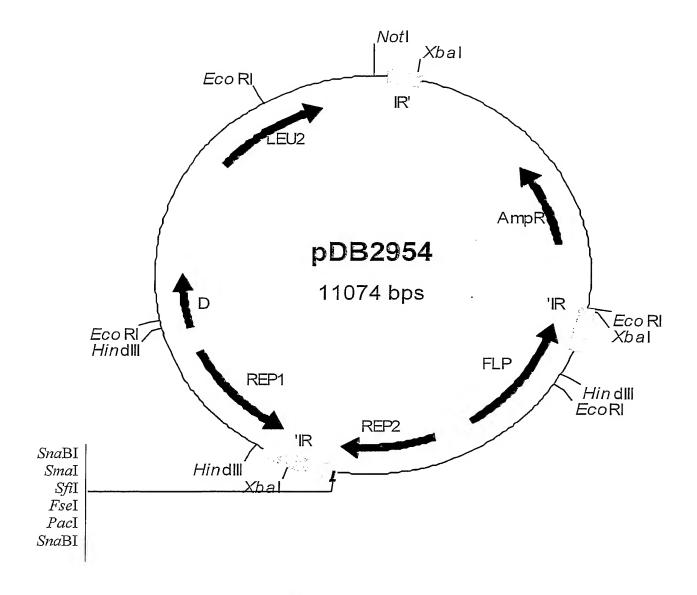


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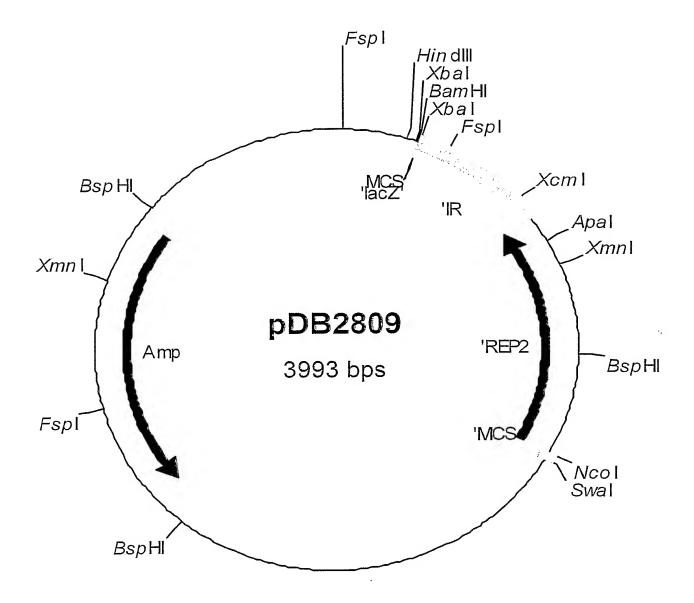


Figure 40

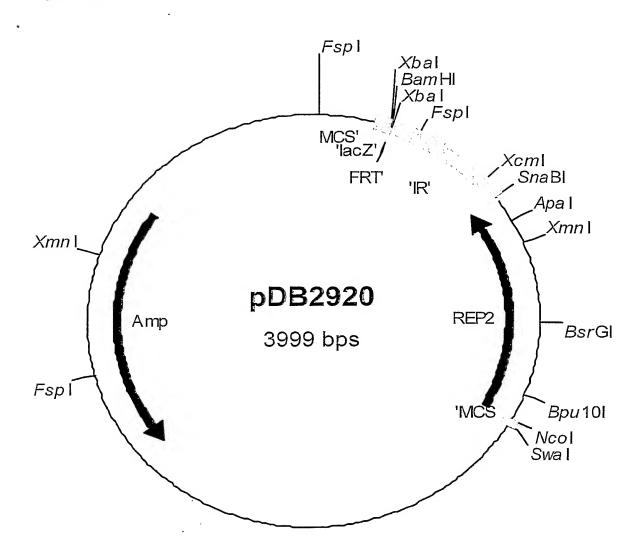


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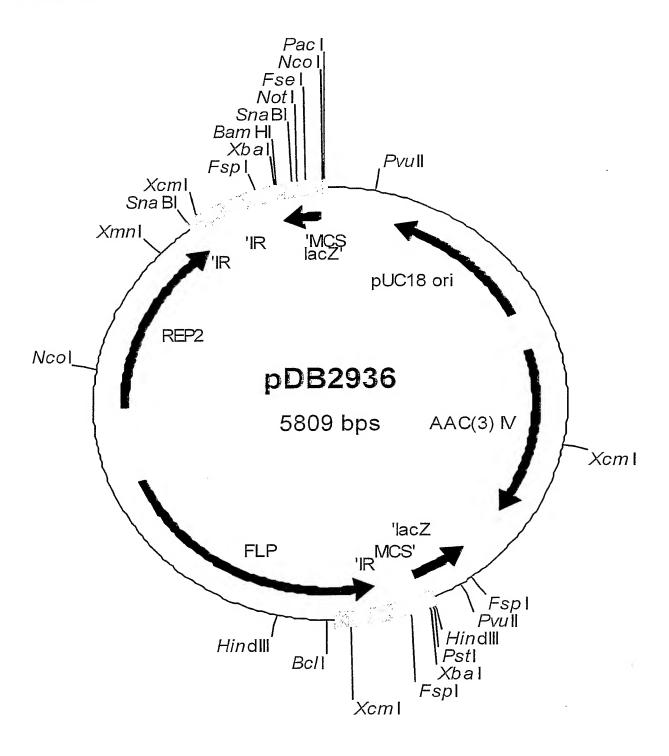


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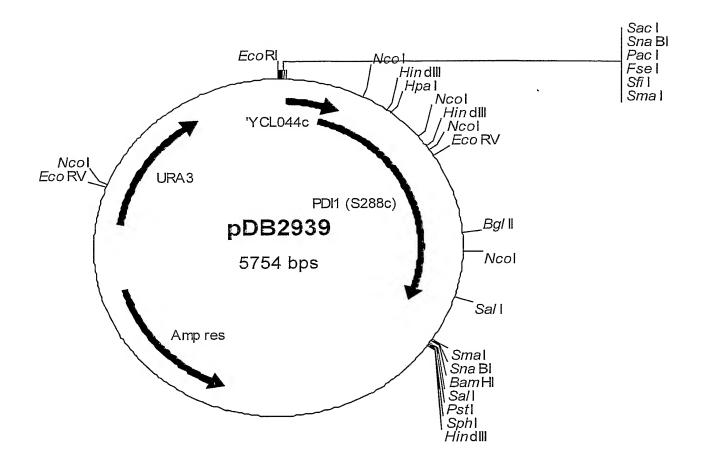


Figure 43

PCR Primers DS248 and DS250 for amplification of S. cerevisiae PDII genes

DS248

SfiI

SacI

PacI

FseI

SnaBI

ECORI

SmaI

5'-GICAGAAIIC GAGCICIACG IATTAAITAA GGCCGGCCAG GCCCGGGCTA GICTCTITIT CCAAITTGCC ACCGIGTAGC AITTTGTIGT-3'

DS250

SnaBI

SmaI

BamHI

5'-GTCAGGATCC TACGTACCCG GGTAAGGCGT TCGTGCAGTG TGACGAATAT AGCG-3'

Figure 44

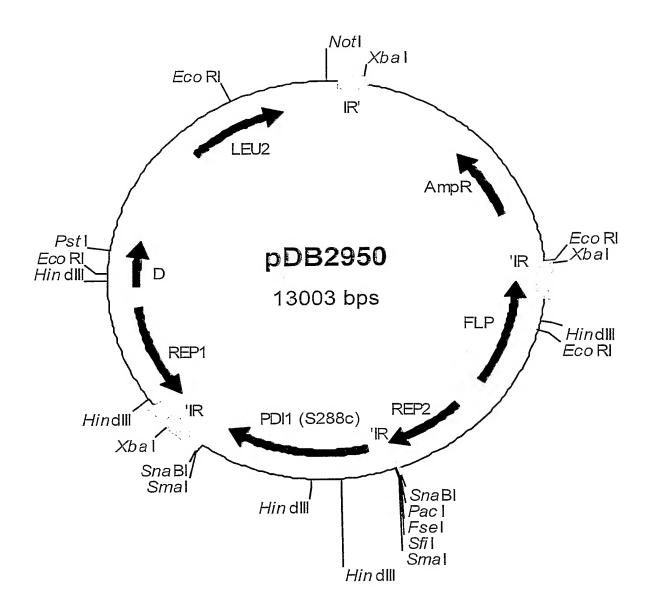


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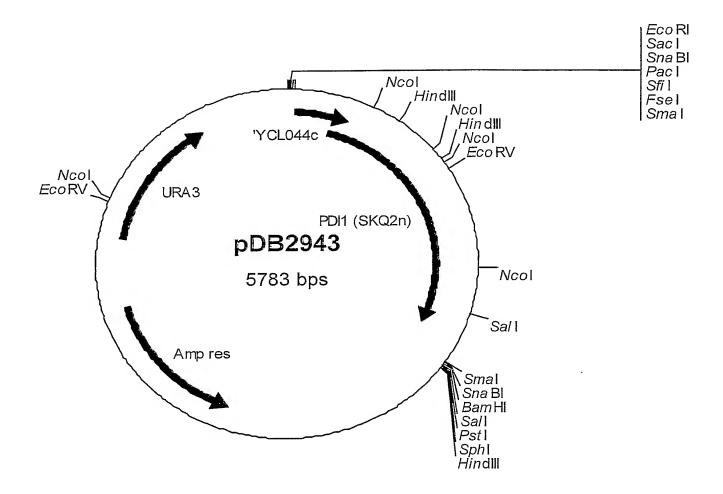


Figure 46

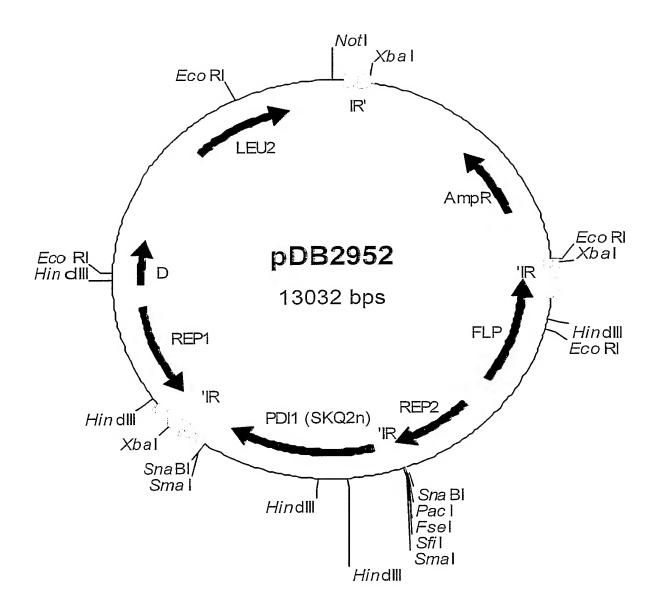
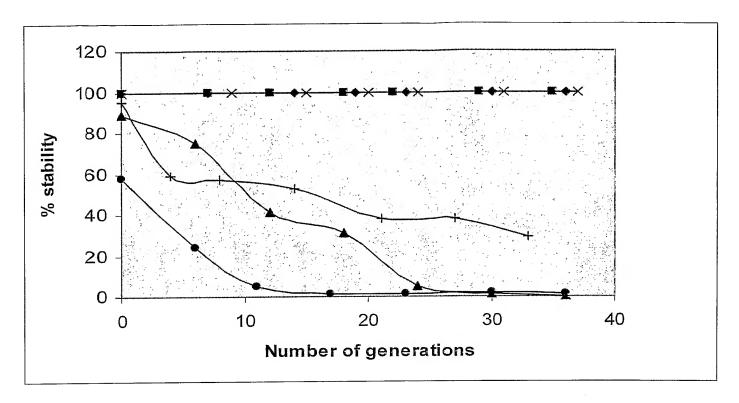
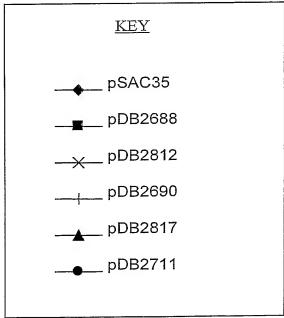
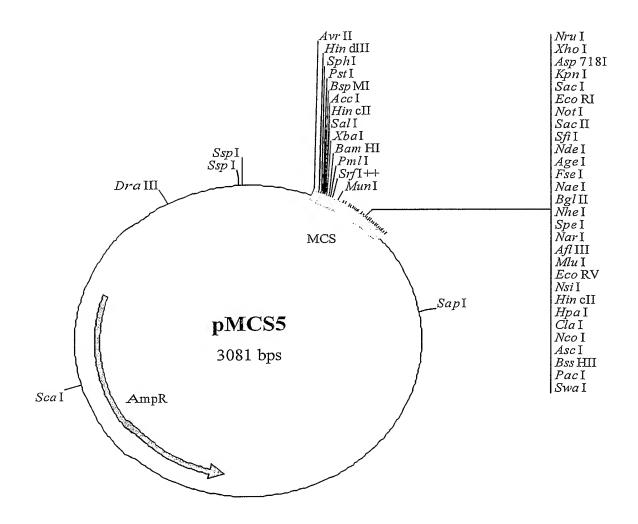
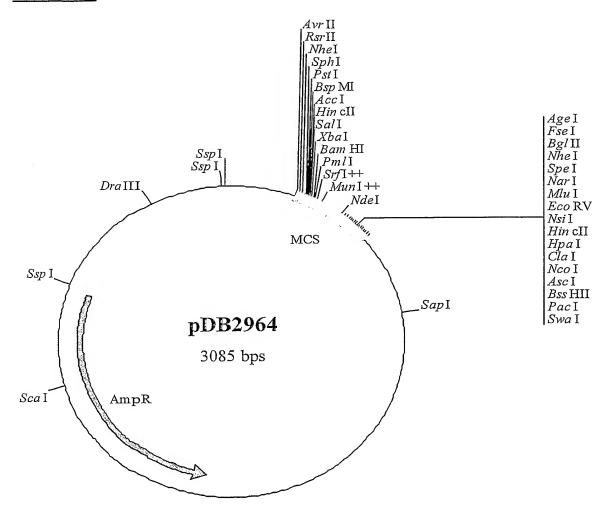


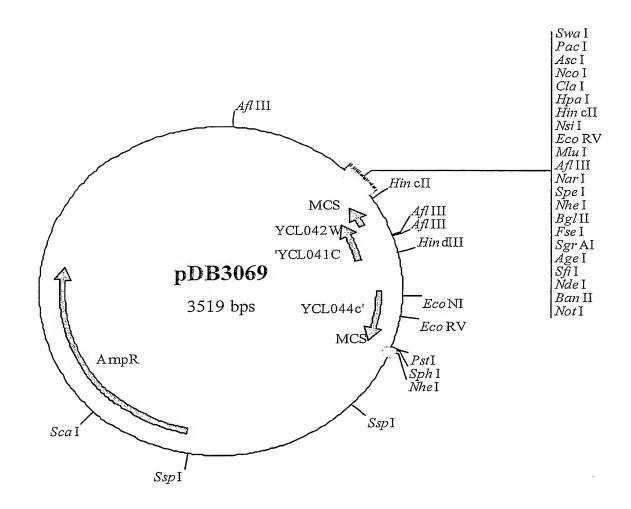
Figure 47

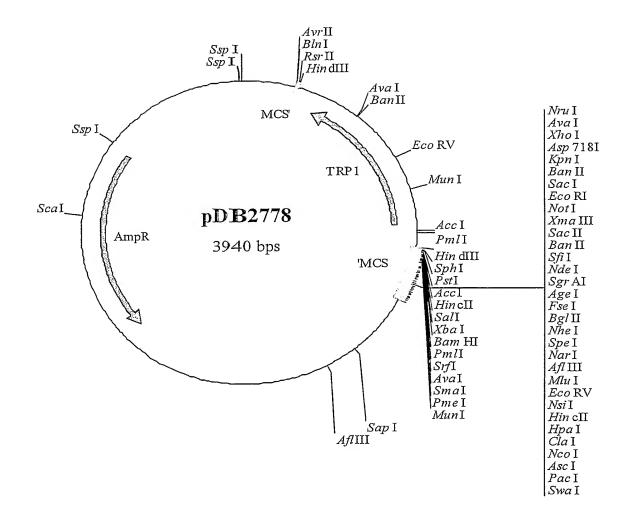


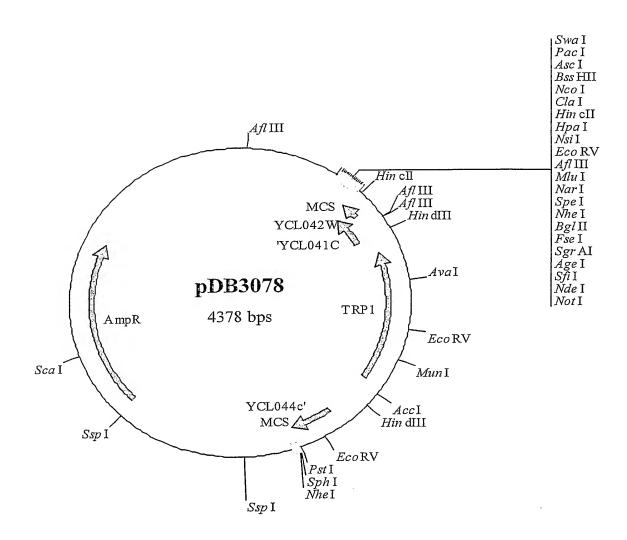


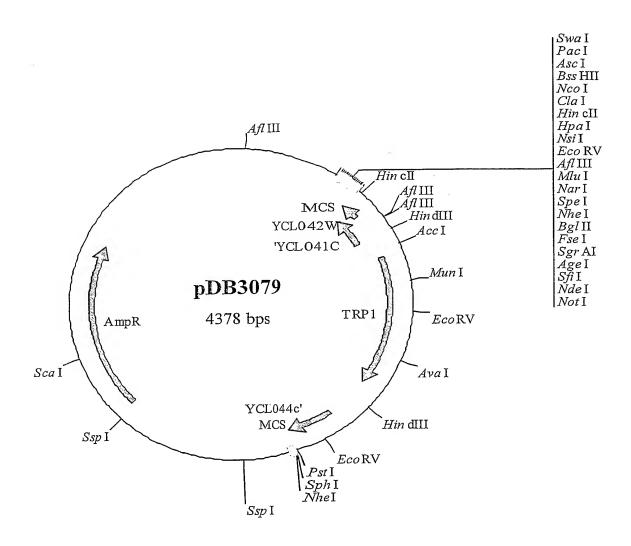


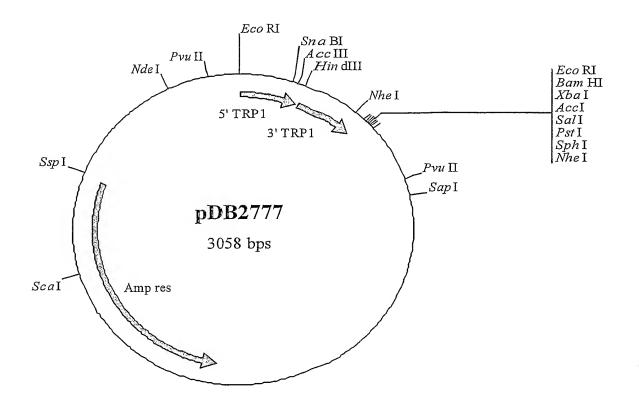












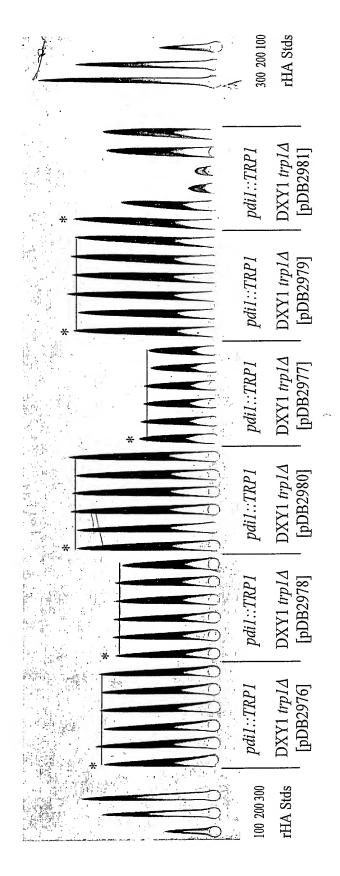


FIGURE 55

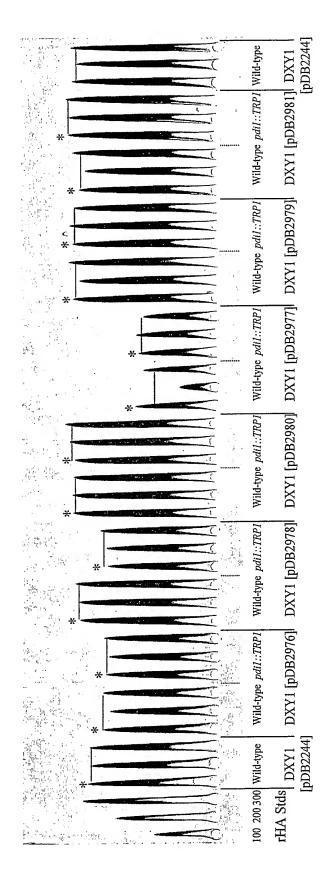


FIGURE 56

Figure 57

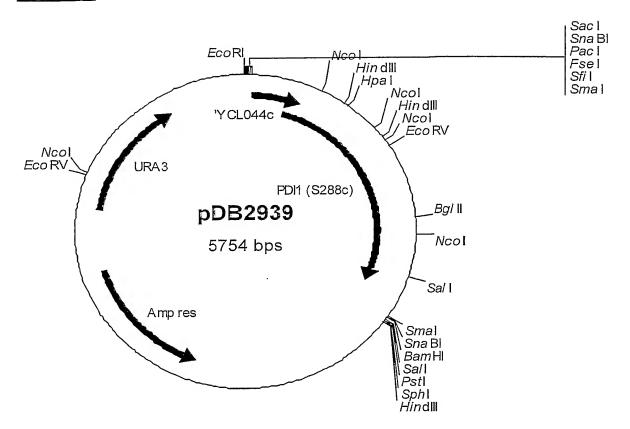


Figure 58

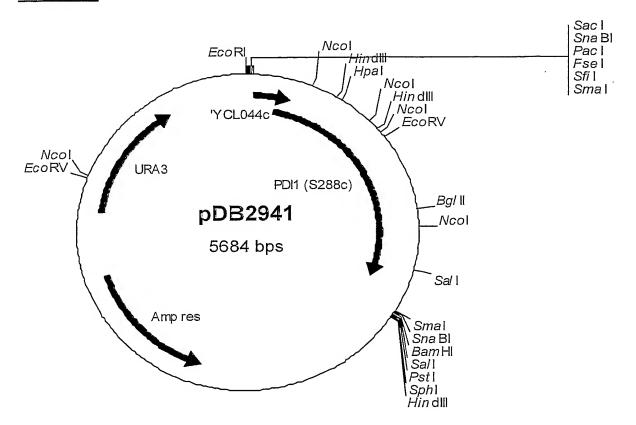


Figure 59

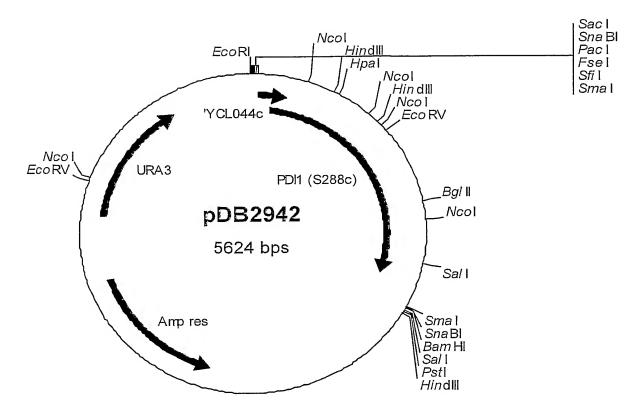


Figure 60

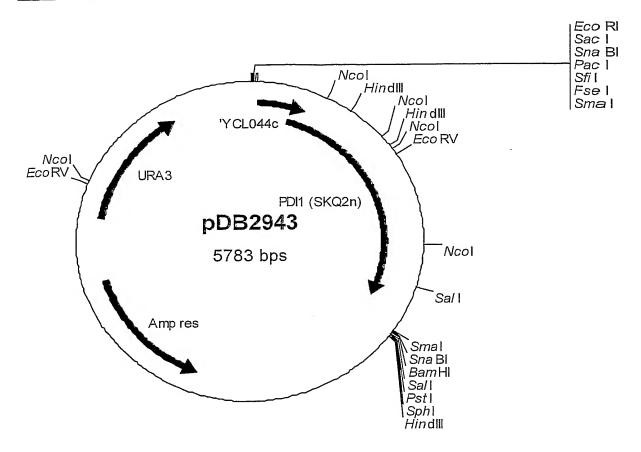


Figure 61

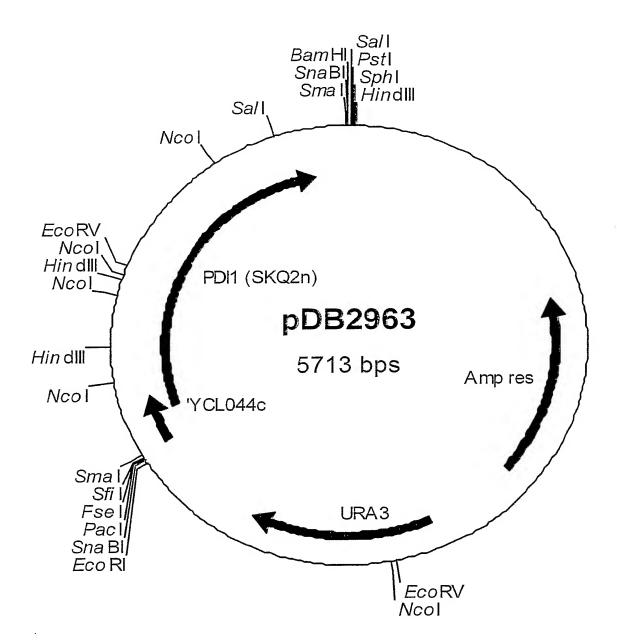


Figure 62

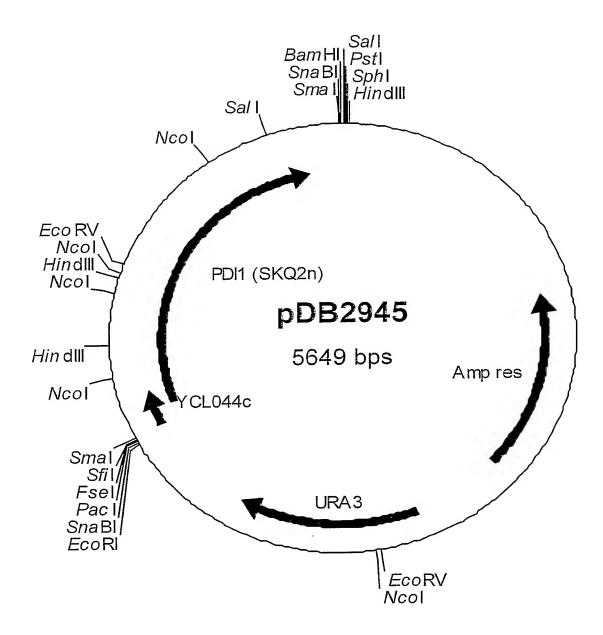


Figure 63

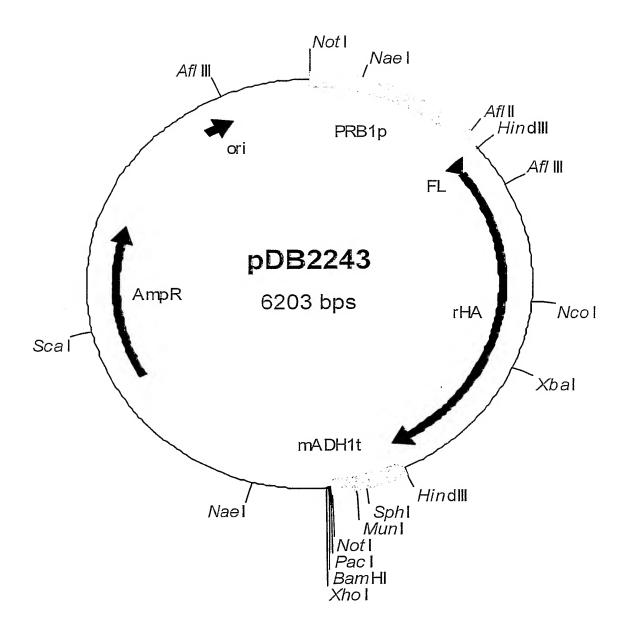
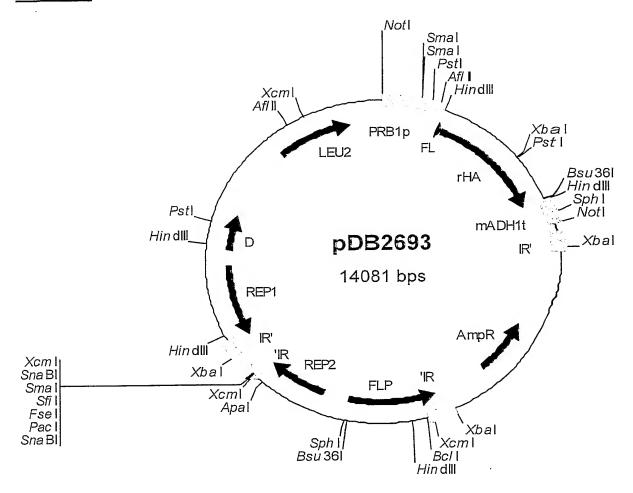
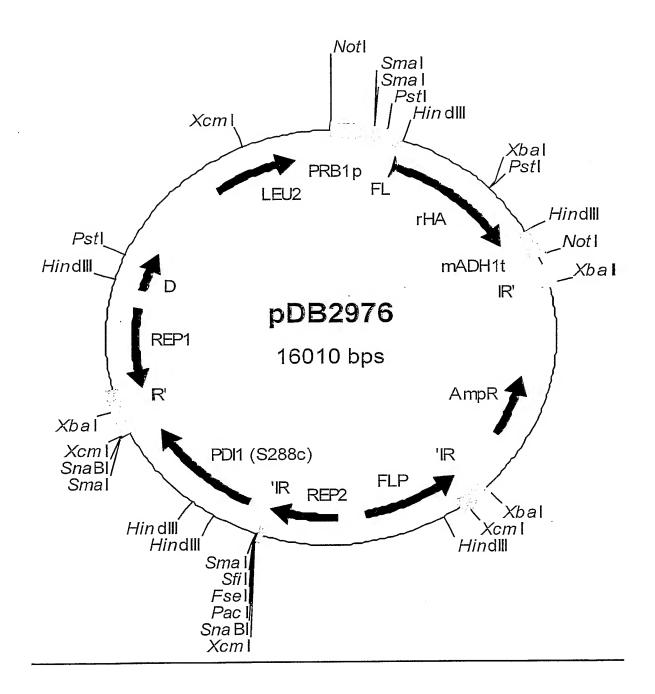
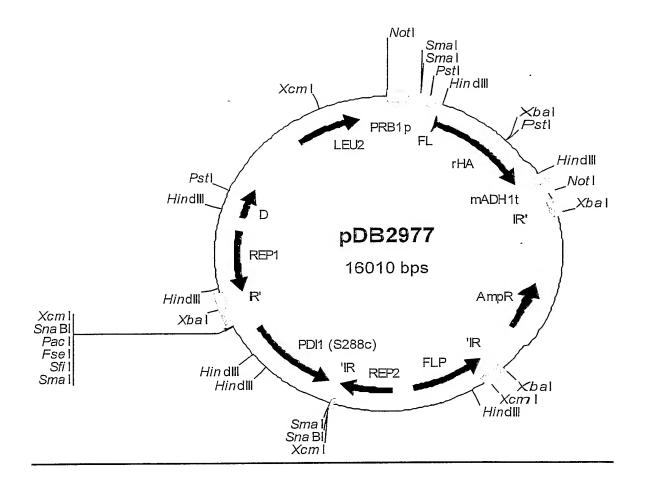
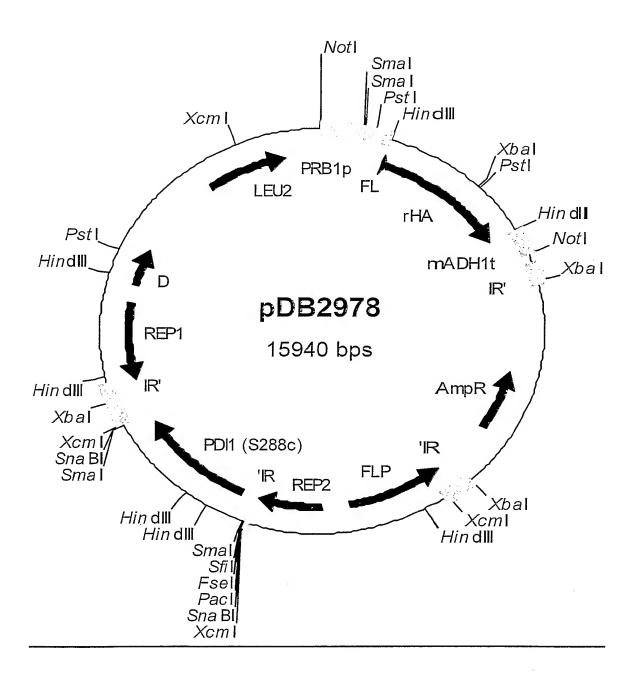


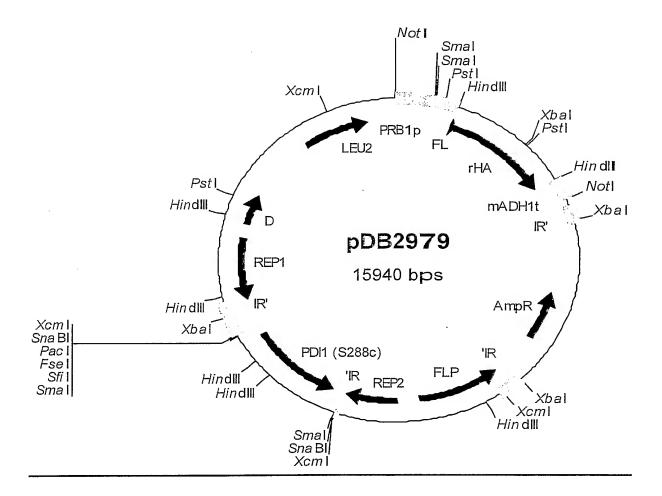
Figure 64











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